

SEQUENCE LISTING

<110> BASF Plant Science GmbH

5

SweTree Technologies AB

<120> POST HARVEST CONTROL OF GENETICALLY MODIFIED CROP GROWTH EM-
10 PLOYING D-AMINO ACID COMPOUNDS

<130> PF 55447 EP

<160> 16

15

<170> PatentIn version 3.1

<210> 1

20 <211> 1160

<212> DNA

<213> Rhodosporidium toruloides

<220>

25 <221> CDS

<222> (1)..(1104)

<223> coding for DAAO

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ctg agc agc gcc ctc atc ctc gct cggt aag ggc tac agc gtg cat att 96
Leu Ser Ser Ala Leu Ile Leu Ala Arg Lys Gly Tyr Ser Val His Ile

35 20 25 30
ctc gcg cgc gac ttg ccg gag gac gtc tcg agc cag act ttc gct tca 144
Leu Ala Arg Asp Leu Pro Glu Asp Val Ser Ser Gln Thr Phe Ala Ser
35 40 45

cct tgg gct ggc aat tgg acg cct ttc atg acg ctt aca gac ggt 192
40 Pro Trp Ala Gly Ala Asn Trp Thr Pro Phe Met Thr Leu Thr Asp Gly

50 55 60

cct cga caa gca aaa tgg gaa gaa tcg act ttc aag aag tgg gtc gag 240
Pro Arg Gln Ala Lys Trp Glu Glu Ser Thr Phe Lys Lys Trp Val Glu
65 70 75 80

45 ttg gtc ccg acg ggc cat gcc atg tgg ctc aag ggg acg agg cgg ttc 288
Leu Val Pro Thr Gly His Ala Met Trp Leu Lys Gly Thr Arg Arg Phe
85 90 95

	gcg cag aac gaa gac ggc ttg ctc ggg cac tgg tac aag gac atc acg Ala Gln Asn Glu Asp Gly Leu Leu Gly His Trp Tyr Lys Asp Ile Thr 100 105 110	336
5	cca aat tac cgc ccc ctc cca tct tcc gaa tgt cca cct ggc gct atc Pro Asn Tyr Arg Pro Leu Pro Ser Ser Glu Cys Pro Pro Gly Ala Ile 115 120 125	384
	ggc gta acc tac gac acc ctc tcc gtc cac gca cca aag tac tgc cag Gly Val Thr Tyr Asp Thr Leu Ser Val His Ala Pro Lys Tyr Cys Gln 130 135 140	432
10	tac ctt gca aga gag ctg cag aag ctc ggc gcg acg ttt gag aga cgg Tyr Leu Ala Arg Glu Leu Gln Lys Leu Gly Ala Thr Phe Glu Arg Arg 145 150 155 160	480
	acc gtt acg tcg ctt gag cag gcg ttc gac ggt gcg gat ttg gtg gtc Thr Val Thr Ser Leu Glu Gln Ala Phe Asp Gly Ala Asp Leu Val Val 165 170 175	528
15	aac gct acg gga ctt ggc gcc aag tcg att gcg ggc atc gac gac caa Asn Ala Thr Gly Leu Gly Ala Lys Ser Ile Ala Gly Ile Asp Asp Gln 180 185 190	576
20	gcc gcc gag cca atc cgc ggg caa acc gtc ctc gtc aag tcc cca tgc Ala Ala Glu Pro Ile Arg Gly Gln Thr Val Leu Val Lys Ser Pro Cys 195 200 205	624
	aag cga tgc acg atg gac tcg tcc gac ccc gct tct ccc gcc tac atc Lys Arg Cys Thr Met Asp Ser Ser Asp Pro Ala Ser Pro Ala Tyr Ile 210 215 220	672
25	att ccc cga cca ggt ggc gaa gtc atc tgc ggc ggg acg tac ggc gtg Ile Pro Arg Pro Gly Gly Glu Val Ile Cys Gly Gly Thr Tyr Gly Val 225 230 235 240	720
	gga gac tgg gac ttg tct gtc aac cca gag acg gtc cag cgg atc ctc Gly Asp Trp Asp Leu Ser Val Asn Pro Glu Thr Val Gln Arg Ile Leu 245 250 255	768
30	aag cac tgc ttg cgc ctc gac ccg acc atc tcg agc gac gga acg atc Lys His Cys Leu Arg Leu Asp Pro Thr Ile Ser Ser Asp Gly Thr Ile 260 265 270	816
	gaa ggc atc gag gtc ctc cgc cac aac gtc ggc ttg cga cct gca cga Glu Gly Ile Glu Val Leu Arg His Asn Val Gly Leu Arg Pro Ala Arg 275 280 285	864
35	cga ggc gga ccc cgc gtt gag gca gaa cgg atc gtc ctg cct ctc gac Arg Gly Gly Pro Arg Val Glu Ala Glu Arg Ile Val Leu Pro Leu Asp 290 295 300	912
40	cgg aca aag tcg ccc ctc tcg ctc ggc agg ggc agc gca cga gcg gcg Arg Thr Lys Ser Pro Leu Ser Leu Gly Arg Gly Ser Ala Arg Ala Ala 305 310 315 320	960
	aag gag aag gag gtc acg ctt gtg cat gcg tat ggc ttc tcg agt gcg Lys Glu Lys Glu Val Thr Leu Val His Ala Tyr Gly Phe Ser Ser Ala 325 330 335	1008
45	gga tac cag cag agt tgg ggc gcg gag gat gtc gcg cag ctc gtc Gly Tyr Gln Gln Ser Trp Gly Ala Ala Glu Asp Val Ala Gln Leu Val	1056

	340	345	350	
gac gag gcg ttc cag cgg tac cac ggc gcg gcg cgg gag tcg aag ttg				1104
Asp Glu Ala Phe Gln Arg Tyr His Gly Ala Ala Arg Glu Ser Lys Leu				
	355	360	365	
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10 <213> Rhodosporidium toruloides				
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20 Leu Ala Arg Asp Leu Pro Glu Asp Val Ser Ser Gln Thr Phe Ala Ser				
	35	40	45	
Pro Trp Ala Gly Ala Asn Trp Thr Pro Phe Met Thr Leu Thr Asp Gly				
	50	55	60	
25 Pro Arg Gln Ala Lys Trp Glu Glu Ser Thr Phe Lys Lys Trp Val Glu.				
	65	70	75	80
Leu Val Pro Thr Gly His Ala Met Trp Leu Lys Gly Thr Arg Arg Phe				
	85	90	95	
30 Ala Gln Asn Glu Asp Gly Leu Leu Gly His Trp Tyr Lys Asp Ile Thr				
	100	105	110	
35 Pro Asn Tyr Arg Pro Leu Pro Ser Ser Glu Cys Pro Pro Gly Ala Ile				
	115	120	125	
Gly Val Thr Tyr Asp Thr Leu Ser Val His Ala Pro Lys Tyr Cys Gln				
	130	135	140	
40 Tyr Leu Ala Arg Glu Leu Gln Lys Leu Gly Ala Thr Phe Glu Arg Arg				
	145	150	155	160
Thr Val Thr Ser Leu Glu Gln Ala Phe Asp Gly Ala Asp Leu Val Val				
	165	170	175	
45 Asn Ala Thr Gly Leu Gly Ala Lys Ser Ile Ala Gly Ile Asp Asp Gln				
	180	185	190	

Ala Ala Glu Pro Ile Arg Gly Gln Thr Val Leu Val Lys Ser Pro Cys
195 200 205

5 Lys Arg Cys Thr Met Asp Ser Ser Asp Pro Ala Ser Pro Ala Tyr Ile
210 215 220

Ile Pro Arg Pro Gly Gly Glu Val Ile Cys Gly Gly Thr Tyr Gly Val
225 230 235 240

10 Gly Asp Trp Asp Leu Ser Val Asn Pro Glu Thr Val Gln Arg Ile Leu
245 250 255

Lys His Cys Leu Arg Leu Asp Pro Thr Ile Ser Ser Asp Gly Thr Ile
15 260 265 270

Glu Gly Ile Glu Val Leu Arg His Asn Val Gly Leu Arg Pro Ala Arg
275 280 285

20 Arg Gly Gly Pro Arg Val Glu Ala Glu Arg Ile Val Leu Pro Leu Asp
290 295 300

Arg Thr Lys Ser Pro Leu Ser Leu Gly Arg Gly Ser Ala Arg Ala Ala
305 310 315 320

25 Lys Glu Lys Glu Val Thr Leu Val His Ala Tyr Gly Phe Ser Ser Ala
325 330 335

Gly Tyr Gln Gln Ser Trp Gly Ala Ala Glu Asp Val Ala Gln Leu Val
30 340 345 350

Asp Glu Ala Phe Gln Arg Tyr His Gly Ala Ala Arg Glu Ser Lys Leu
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<213> *Caenorhabditis elegans*

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<222> (1)..(1002)
<223> coding for DAAO

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Met Ala Asn Ile Ile Pro Lys Ile Ala Ile Ile Gly Glu Gly Val Ile

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				96
	gga tgt act tca gca ctt caa ata tca aaa gct ata cca aat gcg aaa			
	Gly Cys Thr Ser Ala Leu Gln Ile Ser Lys Ala Ile Pro Asn Ala Lys			
	20	25	30	
5	ata act gtg ctc cac gat aaa cca ttt aaa aaa tcg tgc agt gca gga			144
	Ile Thr Val Leu His Asp Lys Pro Phe Lys Lys Ser Cys Ser Ala Gly			
	35	40	45	
	cca gca gga tta ttt aga atc gat tat gag gag aat act gaa tac gga			192
	Pro Ala Gly Leu Phe Arg Ile Asp Tyr Glu Glu Asn Thr Glu Tyr Gly			
10	50	55	60	
	cgt gct tct ttc gcc tgg ttc tca cat ctc tat cgc act aca aaa gga			240
	Arg Ala Ser Phe Ala Trp Phe Ser His Leu Tyr Arg Thr Thr Lys Gly			
	65	70	75	80
	tcc gaa acc ggc gtg aaa tta gtt tct gga cat att caa tcc gac aac			288
15	Ser Glu Thr Gly Val Lys Leu Val Ser Gly His Ile Gln Ser Asp Asn			
	85	90	95	
	ttg gag tca ttg aag caa caa aga gcc tat ggc gat att gtg tac			336
	Leu Glu Ser Leu Lys Gln Gln Arg Ala Tyr Gly Asp Ile Val Tyr			
	100	105	110	
20	aac ttt aga ttc ttg gat gat aga gaa cgg ctg gac att ttt ccc gaa			384
	Asn Phe Arg Phe Leu Asp Asp Arg Glu Arg Leu Asp Ile Phe Pro Glu			
	115	120	125	
	cca tca aag cac tgc att cac tac acc gcc tac gca tca gaa ggt aac			432
	Pro Ser Lys His Cys Ile His Tyr Thr Ala Tyr Ala Ser Glu Gly Asn			
25	130	135	140	
	aag tac gtg cct tat ttg aag aat ttg ctg ctt gag caa aaa atc gag			480
	Lys Tyr Val Pro Tyr Leu Lys Asn Leu Leu Leu Glu Gln Lys Ile Glu			
	145	150	155	160
	ttc aag caa caa gaa gtg acg agt ttg gac gca gtc gcc gac gct ggt			528
30	Phe Lys Gln Gln Glu Val Thr Ser Leu Asp Ala Val Ala Asp Ala Gly			
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	180	185	190	
	180	185	190	
35	tac gat gtt att gta aac tgc gca ggc ttg tac ggt gga aag ttg gct			576
	Tyr Asp Val Ile Val Asn Cys Ala Gly Leu Tyr Gly Gly Lys Leu Ala			
	195	200	205	
	gat gca cca tgg cac aag cac ttc aat tat cga gac ttt act act ttc			624
	Asp Ala Pro Trp His Lys His Phe Asn Tyr Arg Asp Phe Thr Thr Phe			
40	210	215	220	
	aca att cca aaa gag cac agc gtg gtg gtt ggg tcc acc aag cag gac			720
	Thr Ile Pro Lys Glu His Ser Val Val Val Gly Ser Thr Lys Gln Asp			
	225	230	235	240
	aat cga tgg gat ttg gag atc acc gac gag gat aga aat gat att ttg			768
45	Asn Arg Trp Asp Leu Glu Ile Thr Asp Glu Asp Arg Asn Asp Ile Leu			
	245	250	255	
	aaa cga tac att gct tta cat cct gga atg aga gag cca aag att atc			816

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Lys Arg Tyr Ile Ala Leu His Pro Gly Met Arg Glu Pro Lys Ile Ile
 260 265 270
 aaa gaa tgg tca gca ctt cgc ccg gga cgt aag cat gtc aga att gaa
 Lys Glu Trp Ser Ala Leu Arg Pro Gly Arg Lys His Val Arg Ile Glu
 275 280 285
 gcg cag aag agg aca tct gtt gga aac tca aaa gat tat atg gtt gtg
 Ala Gln Lys Arg Thr Ser Val Gly Asn Ser Lys Asp Tyr Met Val Val
 290 295 300
 cat cac tat ggt cac ggg agc aac gga ttc acg ttg ggt tgg gga aca
 10 His His Tyr Gly His Gly Ser Asn Gly Phe Thr Leu Gly Trp Gly Thr
 305 310 315 320
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 <212> PRT
 <213> Caenorhabditis elegans

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 Ile Thr Val Leu His Asp Lys Pro Phe Lys Lys Ser Cys Ser Ala Gly
 35 40 45

30
 Pro Ala Gly Leu Phe Arg Ile Asp Tyr Glu Glu Asn Thr Glu Tyr Gly
 50 55 60

 Arg Ala Ser Phe Ala Trp Phe Ser His Leu Tyr Arg Thr Thr Lys Gly
 35 65 70 75 80

 Ser Glu Thr Gly Val Lys Leu Val Ser Gly His Ile Gln Ser Asp Asn
 85 90 95

40
 Leu Glu Ser Leu Lys Gln Gln Gln Arg Ala Tyr Gly Asp Ile Val Tyr
 100 105 110

 Asn Phe Arg Phe Leu Asp Asp Arg Glu Arg Leu Asp Ile Phe Pro Glu
 115 120 125

45
 Pro Ser Lys His Cys Ile His Tyr Thr Ala Tyr Ala Ser Glu Gly Asn
 130 135 140

Lys Tyr Val Pro Tyr Leu Lys Asn Leu Leu Leu Glu Gln Lys Ile Glu
145 150 155 160

5 Phe Lys Gln Gln Glu Val Thr Ser Leu Asp Ala Val Ala Asp Ala Gly
165 170 175

Tyr Asp Val Ile Val Asn Cys Ala Gly Leu Tyr Gly Gly Lys Leu Ala
180 185 190

10 Gly Asp Asp Asp Thr Cys Tyr Pro Ile Arg Gly Val Ile Leu Glu Val
195 200 205

Asp Ala Pro Trp His His Phe Asn Tyr Arg Asp Phe Thr Thr Phe
15 210 215 220

Thr Ile Pro Lys Glu His Ser Val Val Val Gly Ser Thr Lys Gln Asp
225 230 235 240

20 Asn Arg Trp Asp Leu Glu Ile Thr Asp Glu Asp Arg Asn Asp Ile Leu
245 250 255

Lys Arg Tyr Ile Ala Leu His Pro Gly Met Arg Glu Pro Lys Ile Ile
260 265 270

25 Lys Glu Trp Ser Ala Leu Arg Pro Gly Arg Lys His Val Arg Ile Glu
275 280 285

Ala Gln Lys Arg Thr Ser Val Gly Asn Ser Lys Asp Tyr Met Val Val
30 290 295 300

His His Tyr Gly His Gly Ser Asn Gly Phe Thr Leu Gly Trp Gly Thr
305 310 315 320

35 Ala Ile Glu Ala Thr Lys Leu Val Lys Thr Ala Leu Gly Leu
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40 <212> DNA
<213> Nectria haematococca

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<223> coding for DAAO

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	Val Val Val Gly Ala Gly Val Ile Gly Leu Thr Ser Ala Leu Leu Leu	
	10 20	
10	tcc aag aac aag ggc aac aag atc acc gtc gtg gcc aag cac atg ccc	152
	Ser Lys Asn Lys Gly Asn Lys Ile Thr Val Val Ala Lys His Met Pro	
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	ggc gac tat gac gtt gaa tac gcc tcg cct ttt gct ggt gcc aac cac	200
	Gly Asp Tyr Asp Val Glu Tyr Ala Ser Pro Phe Ala Gly Ala Asn His	
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	tcc ccc atg gcg acg gaa gag agc agc gaa tgg gaa cgt cgc act tgg	248
	Ser Pro Met Ala Thr Glu Glu Ser Ser Glu Trp Glu Arg Arg Thr Trp	
	55 60 65	
	tac gag ttt aag aga ctg gtc gag gag gtc cct gag gcc ggt gtt cat	296
20	Tyr Glu Phe Lys Arg Ile Val Glu Glu Val Pro Glu Ala Gly Val His	
	70 75 80 85	
	ttc cag aag tct cgc atc cag agg cgc aat gtg gac act gaa aag gcg	344
	Phe Gln Lys Ser Arg Ile Gln Arg Arg Asn Val Asp Thr Glu Lys Ala	
	90 95 100	
25	cag agg tct ggt ttc cca gac gcc ctc ttc tcg aaa gaa ccc tgg ttc	392
	Gln Arg Ser Gly Phe Pro Asp Ala Leu Phe Ser Lys Glu Pro Trp Phe	
	105 110 115	
	aag aac atg ttt gag gac ttc cgt gag cag cac cct agc gag gtc atc	440
	Lys Asn Met Phe Glu Asp Phe Arg Glu Gln His Pro Ser Glu Val Ile	
30	120 125 130	
	ccc ggt tac gac tct ggc tgc gag ttc aca tcg gtg tgc atc aac acg	488
	Pro Gly Tyr Asp Ser Gly Cys Glu Phe Thr Ser Val Cys Ile Asn Thr	
	135 140 145	
	gcc atc tac ctc ccc tgg ctc ctc ggc cag tgc atc aag aat ggc gtc	536
35	Ala Ile Tyr Leu Pro Trp Leu Leu Gly Gln Cys Ile Lys Asn Gly Val	
	150 155 160 165	
	atc gtc aag cgc gcc atc ctc aac gac att agc gag gcc aag aag ctg	584
	Ile Val Lys Arg Ala Ile Leu Asn Asp Ile Ser Glu Ala Lys Lys Leu	
	170 175 180	
40	agc cac gcg ggc aag acg ccc aat atc atc gtc aac gcc acg ggt ctc	632
	Ser His Ala Gly Lys Thr Pro Asn Ile Ile Val Asn Ala Thr Gly Leu	
	185 190 195	
	ggc tcc tac aag ctg ggc ggt gtc gag gac aag acc atg gcg cct gcg	680
	Gly Ser Tyr Lys Leu Gly Gly Val Glu Asp Lys Thr Mét Ala Pro Ala	
45	200 205 210	
	cgg gga cag att gtg gtt gtg cgc aac gag agc agc ccc atg ctc ctc	728
	Arg Gly Gln Ile Val Val Arg Asn Glu Ser Ser Pro Met Leu Leu	

	215	220	225	
	act tca ggt gtc gag gac ggc ggt gct gat gtc atg tac ttg atg cag			776
	Thr Ser Gly Val Glu Asp Gly Gly Ala Asp Val Met Tyr Leu Met Gln			
	230	235	240	245
5	cga gca gct ggc ggt ggc acc atc ctg ggc ggt acc tac gac gtt ggc			824
	Arg Ala Ala Gly Gly Thr Ile Leu Gly Gly Thr Tyr Asp Val Gly			
	250	255	260	
	aac tgg gag tct cag cca gac ccc aac atc gcg aat cgc atc atg cag			872
	Asn Trp Glu Ser Gln Pro Asp Pro Asn Ile Ala Asn Arg Ile Met Gln			
10	265	270	275	
	cgc atc gtc gag gtg cgg ccc gag att gcc aac ggc aag ggc gtc aag			920
	Arg Ile Val Glu Val Arg Pro Glu Ile Ala Asn Gly Lys Gly Val Lys			
	280	285	290	
	ggg ctg agc gtg atc cga cac gcc gtc ggc atg cgg ccg tgg cga aag			968
15	Gly Leu Ser Val Ile Arg His Ala Val Gly Met Arg Pro Trp Arg Lys			
	295	300	305	
	gac gga gtc agg atc gag gag aag ctg gat gat gag act tgg atc			1016
	Asp Gly Val Arg Ile Glu Glu Glu Lys Leu Asp Asp Glu Thr Trp Ile			
	310	315	320	325
20	gtg cac aac tac gga cac tct gga tgg ggt tac cag ggt tcg tat ggt			1064
	Val His Asn Tyr Gly His Ser Gly Trp Gly Tyr Gln Gly Ser Tyr Gly			
	330	335	340	
	tgt gct gag aat gta gtc cag ttg gtt gac aag gtc ggc aag gcg gcc			1112
	Cys Ala Glu Asn Val Val Gln Leu Val Asp Lys Val Gly Lys Ala Ala			
25	345	350	355	
	aag tct aag ctg tagtgaaaa ggcctgaatg agtaatagta attggatatt			1164
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	20	25	30	
	Ala Lys His Met Pro Gly Asp Tyr Asp Val Glu Tyr Ala Ser Pro Phe			
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45	Ala Gly Ala Asn His Ser Pro Met Ala Thr Glu Glu Ser Ser Glu Trp			
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Glu Arg Arg Thr Trp Tyr Glu Phe Lys Arg Leu Val Glu Glu Val Pro
65 70 75 80

5 Glu Ala Gly Val His Phe Gln Lys Ser Arg Ile Gln Arg Arg Asn Val
85 90 95

Asp Thr Glu Lys Ala Gln Arg Ser Gly Phe Pro Asp Ala Leu Phe Ser
100 105 110

10 Lys Glu Pro Trp Phe Lys Asn Met Phe Glu Asp Phe Arg Glu Gln His
115 120 125

Pro Ser Glu Val Ile Pro Gly Tyr Asp Ser Gly Cys Glu Phe Thr Ser
15 130 135 140

Val Cys Ile Asn Thr Ala Ile Tyr Leu Pro Trp Leu Leu Gly Gln Cys
145 150 155 160

20 Ile Lys Asn Gly Val Ile Val Lys Arg Ala Ile Leu Asn Asp Ile Ser
165 170 175

Glu Ala Lys Lys Leu Ser His Ala Gly Lys Thr Pro Asn Ile Ile Val
180 185 190

25 Asn Ala Thr Gly Leu Gly Ser Tyr Lys Leu Gly Gly Val Glu Asp Lys
195 200 205

Thr Met Ala Pro Ala Arg Gly Gln Ile Val Val Val Arg Asn Glu Ser
30 210 215 220

Ser Pro Met Leu Leu Thr Ser Gly Val Glu Asp Gly Gly Ala Asp Val
225 230 235 240

35 Met Tyr Leu Met Gln Arg Ala Ala Gly Gly Thr Ile Leu Gly Gly
245 250 255

Thr Tyr Asp Val Gly Asn Trp Glu Ser Gln Pro Asp Pro Asn Ile Ala
260 265 270

40 Asn Arg Ile Met Gln Arg Ile Val Glu Val Arg Pro Glu Ile Ala Asn
275 280 285

Gly Lys Gly Val Lys Gly Leu Ser Val Ile Arg His Ala Val Gly Met
45 290 295 300

Arg Pro Trp Arg Lys Asp Gly Val Arg Ile Glu Glu Glu Lys Leu Asp

305	310	315	320
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Asp Glu Thr Trp Ile Val His Asn Tyr Gly His Ser Gly Trp Gly Tyr			
325	330	335	

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Gln Gly Ser Tyr Gly Cys Ala Glu Asn Val Val Gln Leu Val Asp Lys			
340	345	350	

Val Gly Lys Ala Ala Lys Ser Lys Leu			
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25 1 5 10 15			
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gct ctt caa ctt ctt cgt aaa gga cat gag gtt aca att gtg tcc gag			96
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35 . . . 40 . . . 45			

gcc aac tgg ctc aca ttt tac gat gga ggc aag tta gcc gac tac gat			192
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50 . . . 55 . . . 60			

35 gcc gtc tct tat cct atc ttg cga gag ctg gct cga agc agc ccc gag			240
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65 . . . 70 . . . 75 . . . 80			

gct gga att cga ctc atc agc caa cgc tcc cat gtt ctc aag cgt gat			288
Ala Gly Ile Arg Leu Ile Ser Gln Arg Ser His Val Leu Lys Arg Asp			
85 . . . 90 . . . 95			

40 ctt cct aaa ctg gaa gtt gcc atg tcg gcc atc tgt caa cgc aat ccc			336
Leu Pro Lys Leu Glu Val Ala Met Ser Ala Ile Cys Gln Arg Asn Pro			
100 . . . 105 . . . 110			

45 tgg ttc aaa aac aca gtc gat tct ttc gag att atc gag gac agg tcc			384
Trp Phe Lys Asn Thr Val Asp Ser Phe Glu Ile Ile Glu Asp Arg Ser			
115 . . . 120 . . . 125			

agg att gtc cac gat gat gtg gct tat cta gtc gaa ttt cgt tcc gtt			432
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	Arg Ile Val His Asp Asp Val Ala Tyr Leu Val Glu Phe Arg Ser Val			
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	tgt atc cac acc gga gtc tac ttg aac tgg ctg atg tcc caa tgc tta			480
	Cys Ile His Thr Gly Val Tyr Leu Asn Trp Leu Met Ser Gln Cys Leu			
5	145	150	155	160
	tcg ctc ggc gcc acg gtg gtt aaa cgt cga gtg aac cat atc aag gat			528
	Ser Leu Gly Ala Thr Val Val Lys Arg Arg Val Asn His Ile Lys Asp			
	165	170	175	
	gcc aat tta cta cac tcc tca gga tca cgc ccc gac gtg att gtc aac			576
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	180	185	190	
	tgt agt ggt ctc ttt gcc cgg ttc ttg gga ggc gtc gag gac aag aag			624
	Cys Ser Gly Leu Phe Ala Arg Phe Leu Gly Gly Val Glu Asp Lys Lys			
	195	200	205	
15	atg tac cct att cga gga caa gtc gtc ctt gtt cga aac tct ctt cct			672
	Met Tyr Pro Ile Arg Gly Gln Val Val Leu Val Arg Asn Ser Leu Pro			
	210	215	220	
	ttt atg gcc tcc ttt tcc agc act cct gaa aaa gaa aat gaa gac gaa			720
	Phe Met Ala Ser Phe Ser Ser Thr Pro Glu Lys Glu Asn Glu Asp Glu			
20	225	230	235	240
	gct cta tat atc atg acc cga ttc gat ggt act tct atc att ggc ggt			768
	Ala Leu Tyr Ile Met Thr Arg Phe Asp Gly Thr Ser Ile Ile Gly Gly			
	245	250	255	
	tgt ttc caa ccc aac aac tgg tca tcc gaa ccc gat cct tct ctc acc			816
25	Cys Phe Gln Pro Asn Asn Trp Ser Ser Glu Pro Asp Pro Ser Leu Thr			
	260	265	270	
	cat cga atc ctg tct aga gcc ctc gac cga ttc ccg gaa ctg acc aaa			864
	His Arg Ile Leu Ser Arg Ala Leu Asp Arg Phe Pro Glu Leu Thr Lys			
	275	280	285	
30	gat ggc cct ctt gac att gtg cgc gaa tgc gtt ggc cac cgt cct ggt			912
	Asp Gly Pro Leu Asp Ile Val Arg Glu Cys Val Gly His Arg Pro Gly			
	290	295	300	
	aga gag ggc ggt ccc cga gta gaa tta gag aag atc ccc ggc gtt ggc			960
	Arg Glu Gly Pro Arg Val Glu Leu Glu Lys Ile Pro Gly Val Gly			
35	305	310	315	320
	ttt gtt gtc cat aac tat ggt gcc gcc ggt gct ggt tac caa tcc tct			1008
	Phe Val Val His Asn Tyr Gly Ala Ala Gly Ala Gly Tyr Gln Ser Ser			
	325	330	335	
	tac ggc atg gct gat gaa gct gtt tct tac gtc gaa aga gct ctt act			1056
40	Tyr Gly Met Ala Asp Glu Ala Val Ser Tyr Val Glu Arg Ala Leu Thr			
	340	345	350	
	cgt cca aac ctt tag			1071
	Arg Pro Asn Leu			
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<212> PRT

<213> Trigonopsis variabilis

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5 Met Ala Lys Ile Val Val Ile Gly Ala Gly Val Ala Gly Leu Thr Thr
1 5 10 15

Ala Leu Gln Leu Leu Arg Lys Gly His Glu Val Thr Ile Val Ser Glu
20 25 30

10 Phe Thr Pro Gly Asp Leu Ser Ile Gly Tyr Thr Ser Pro Trp Ala Gly
35 40 45

Ala Asn Trp Leu Thr Phe Tyr Asp Gly Gly Lys Leu Ala Asp Tyr Asp
15 50 55 60

Ala Val Ser Tyr Pro Ile Leu Arg Glu Leu Ala Arg Ser Ser Pro Glu
65 70 75 80

20 Ala Gly Ile Arg Leu Ile Ser Gln Arg Ser His Val Leu Lys Arg Asp
85 90 95

Leu Pro Lys Leu Glu Val Ala Met Ser Ala Ile Cys Gln Arg Asn Pro
100 105 110

25 Trp Phe Lys Asn Thr Val Asp Ser Phe Glu Ile Ile Glu Asp Arg Ser
115 120 125

Arg Ile Val His Asp Asp Val Ala Tyr Leu Val Glu Phe Arg Ser Val
30 130 135 140

Cys Ile His Thr Gly Val Tyr Leu Asn Trp Leu Met Ser Gln Cys Leu
145 150 155 160

35 Ser Leu Gly Ala Thr Val Val Lys Arg Arg Val Asn His Ile Lys Asp
165 170 175

Ala Asn Leu Leu His Ser Ser Gly Ser Arg Pro Asp Val Ile Val Asn
180 185 190

40 Cys Ser Gly Leu Phe Ala Arg Phe Leu Gly Gly Val Glu Asp Lys Lys
195 200 205

Met Tyr Pro Ile Arg Gly Gln Val Val Leu Val Arg Asn Ser Leu Pro
45 210 215 220

Phe Met Ala Ser Phe Ser Ser Thr Pro Glu Lys Glu Asn Glu Asp Glu

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225	230	235	240
Ala Leu Tyr Ile Met Thr Arg Phe Asp Gly Thr Ser Ile Ile Gly Gly			
	245	250	255
5			
Cys Phe Gln Pro Asn Asn Trp Ser Ser Glu Pro Asp Pro Ser Leu Thr			
	260	265	270
His Arg Ile Leu Ser Arg Ala Leu Asp Arg Phe Pro Glu Leu Thr Lys			
10	275	280	285
Asp Gly Pro Leu Asp Ile Val Arg Glu Cys Val Gly His Arg Pro Gly			
	290	295	300
15	Arg Glu Gly Gly Pro Arg Val Glu Leu Glu Lys Ile Pro Gly Val Gly		
	305	310	315
	320		
Phe Val Val His Asn Tyr Gly Ala Ala Gly Ala Gly Tyr Gln Ser Ser			
	325	330	335
20	Tyr Gly Met Ala Asp Glu Ala Val Ser Tyr Val Glu Arg Ala Leu Thr		
	340	345	350
Arg Pro Asn Leu			
25	355		
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30	<213> Schizosaccharomyces pombe.		
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	Arg Asp Ile Val Ile Val Gly Ala Gly Val		
40	1	5	10
att gga ttg acc act gct tgg att ctt tca gac ttg ggt ctt gct cct			
	Ile Gly Leu Thr Thr Ala Trp Ile Leu Ser Asp Leu Gly Leu Ala Pro		
	15	20	25
cgt att aag gtg att gcc aag tat acg cct gaa gat cgt tct gta gaa			
45	Arg Ile Lys Val Ile Ala Lys Tyr Thr Pro Glu Asp Arg Ser Val Glu		
	30	35	40
tac act tcc cct tgg gct ggc gca aat ttc tgt agc att tct gct act			
			195

Tyr	Thr	Ser	Pro	Trp	Ala	Gly	Ala	Asn	Phe	Cys	Ser	Ile	Ser	Ala	Thr		
45							50					55					
gat	gac	aat	gct	ttg	cgc	tgg	gat	aaa	atc	act	tac	cat	cgt	ttc	gcc	243	
Asp	Asp	Asn	Ala	Leu	Arg	Trp	Asp	Lys	Ile	Thr	Tyr	His	Arg	Phe	Ala		
5	60						65				70						
tac	ttg	gcg	aaa	act	cgt	cct	gaa	gca	gga	atc	cgt	ttt	gct	gat	ctt	291	
Tyr	Leu	Ala	Lys	Thr	Arg	Pro	Glu	Ala	Gly	Ile	Arg	Phe	Ala	Asp	Leu		
75							80			85			90				
cga	gaa	ttg	tgg	gag	tac	gag	ccg	aaa	cac	gac	aaa	atc	aga	tcc	tgg	339	
10	Arg	Glu	Leu	Trp	Glu	Tyr	Glu	Pro	Lys	His	Asp	Lys	Ile	Arg	Ser	Trp	
							95			100			105				
aat	acc	tat	gtc	aga	gat	ttc	aaa	gtt	atc	cct	gaa	aaa	gat	ctt	cca	387	
Asn	Thr	Tyr	Val	Arg	Asp	Phe	Lys	Val	Ile	Pro	Glu	Lys	Asp	Leu	Pro		
							110			115			120				
15	gga	gaa	tgt	atc	tac	gga	cat	aag	gcc	acc	acc	ttt	tta	atc	aac	gct	435
Gly	Glu	Cys	Ile	Tyr	Gly	His	Lys	Ala	Thr	Thr	Phe	Leu	Ile	Asn	Ala		
							125			130			135				
cct	cat	tac	ttg	aat	tat	atg	tac	aag	ctg	ctc	att	gaa	gct	ggc	gtc	483	
Pro	His	Tyr	Leu	Asn	Tyr	Met	Tyr	Lys	Leu	Leu	Ile	Glu	Ala	Gly	Val		
20	140						145				150						
gaa	ttt	gaa	aag	aaa	gaa	ttg	agt	cac	atc	aaa	gag	act	gtc	gaa	gaa	531	
Glu	Phe	Glu	Lys	Lys	Glu	Ieu	Ser	His	Ile	Lys	Glu	Thr	Val	Glu	Glu		
						155			160		165		170				
act	cca	gaa	gct	tca	gta	gta	ttt	aat	tgc	act	ggt	ctc	tgg	gct	tcc	579	
25	Thr	Pro	Glu	Ala	Ser	Val	Val	Phe	Asn	Cys	Thr	Gly	Leu	Trp	Ala	Ser	
							175			180			185				
aaa	ttg	ggt	ggc	gtt	gaa	gac	ccg	gac	gtt	tat	ccg	act	cgt	gga	cat	627	
Lys	Leu	Gly	Gly	Val	Glu	Asp	Pro	Asp	Val	Tyr	Pro	Thr	Arg	Gly	His		
						190			195			200					
30	gtt	gtt	ttg	gtt	aag	gct	cct	cat	gta	aca	gaa	act	cgc	att	ttg	aat	675
Val	Val	Leu	Val	Lys	Ala	Pro	His	Val	Thr	Glu	Thr	Arg	Ile	Leu	Asn		
						205			210			215					
ggc	aag	aac	tct	gat	acc	tat	att	att	cct	cgt	ccc	tta	aat	ggt	gga	723	
Gly	Lys	Asn	Ser	Asp	Thr	Tyr	Ile	Ile	Pro	Arg	Pro	Leu	Asn	Gly	Gly		
35	220						225				230						
gtc	att	tgc	ggc	ggt	ttc	atg	caa	cca	gga	aac	tgg	gat	cgt	gaa	att	771	
Val	Ile	Cys	Gly	Gly	Phe	Met	Gln	Pro	Gly	Asn	Trp	Asp	Arg	Glu	Ile		
						235			240		245		250				
cac	cct	gaa	gac	act	ttg	gat	atc	ctt	aag	aga	aca	tcg	gct	ttg	atg	819	
40	His	Pro	Glu	Asp	Thr	Leu	Asp	Ile	Leu	Lys	Arg	Thr	Ser	Ala	Leu	Met	
							255			260			265				
cca	gaa	ttg	tgc	cac	ggc	aag	ggt	ccg	gag	ggt	gct	gaa	att	att	caa	867	
Pro	Glu	Leu	Phe	His	Gly	Lys	Gly	Pro	Glu	Gly	Ala	Glu	Ile	Ile	Gln		
						270			275			280					
45	gaa	tgt	gtc	gga	ttc	cgt	cct	tct	cga	aag	ggt	ggt	gcc	cgc	gta	gag	915
Glu	Cys	Val	Gly	Phe	Arg	Pro	Ser	Arg	Lys	Gly	Gly	Ala	Arg	Val	Glu		
							285			290			295				

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ctt gat gtt gtt ccc ggc acc tca gtc ccc ctt gtt cat gat tac ggt 963
Leu Asp Val Val Pro Gly Thr Ser Val Pro Leu Val His Asp Tyr Gly.
300 305 310

gct tct ggc aca gga tac caa gct ggt tat ggt atg gct ctt gac tct 1011
5 Ala Ser Gly Thr Gly Tyr Gln Ala Gly Tyr Gly Met Ala Leu Asp Ser
315 320 325 330

gtc atg ttg gct ctt cct aaa atc aaa ttg gcttag 1047
Val Met Leu Ala Leu Pro Lys Ile Lys Leu
335 340

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<213> Schizosaccharomyces pombe

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20 Trp Ile Leu Ser Asp Leu Gly Leu Ala Pro Arg Ile Lys Val Ile Ala
20 25 30

Lys Tyr Thr Pro Glu Asp Arg Ser Val Glu Tyr Thr Ser Pro Trp Ala
35 40 45

25 Gly Ala Asn Phe Cys Ser Ile Ser Ala Thr Asp Asp Asn Ala Leu Arg
50 55 60

Trp Asp Lys Ile Thr Tyr His Arg Phe Ala Tyr Leu Ala Lys Thr Arg
30 65 70 75 80

Pro Glu Ala Gly Ile Arg Phe Ala Asp Leu Arg Glu Leu Trp Glu Tyr
85 90 95

35 Glu Pro Lys His Asp Lys Ile Arg Ser Trp Asn Thr Tyr Val Arg Asp
100 105 110

Phe Lys Val Ile Pro Glu Lys Asp Leu Pro Gly Glu Cys Ile Tyr Gly
115 120 125

40 His Lys Ala Thr Thr Phe Leu Ile Asn Ala Pro His Tyr Leu Asn Tyr
130 135 140

Met Tyr Lys Leu Leu Ile Glu Ala Gly Val Glu Phe Glu Lys Lys Glu
45 145 150 155 160

Leu Ser His Ile Lys Glu Thr Val Glu Glu Thr Pro Glu Ala Ser Val

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165 170 175

Val Phe Asn Cys Thr Gly Leu Trp Ala Ser Lys Leu Gly Gly Val Glu
180 185 190

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Asp Pro Asp Val Tyr Pro Thr Arg Gly His Val Val Leu Val Lys Ala
195 200 205

Pro His Val Thr Glu Thr Arg Ile Leu Asn Gly Lys Asn Ser Asp Thr
10 210 215 220

Tyr Ile Ile Pro Arg Pro Leu Asn Gly Gly Val Ile Cys Gly Gly Phe
225 230 235 240

15 Met Gln Pro Gly Asn Trp Asp Arg Glu Ile His Pro Glu Asp Thr Leu
245 250 255

Asp Ile Leu Lys Arg Thr Ser Ala Leu Met Pro Glu Leu Phe His Gly
260 265 270

20

Lys Gly Pro Glu Gly Ala Glu Ile Ile Gln Glu Cys Val Gly Phe Arg
275 280 285

25

Pro Ser Arg Lys Gly Gly Ala Arg Val Glu Leu Asp Val Val Pro Gly
290 295 300

Thr Ser Val Pro Leu Val His Asp Tyr Gly Ala Ser Gly Thr Gly Tyr
305 310 315 320

30

Gln Ala Gly Tyr Gly Met Ala Leu Asp Ser Val Met Leu Ala Leu Pro
325 330 335

Lys Ile Lys Leu
340

35

<210> 11
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<212> DNA
<213> Streptomyces coelicolor

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<222> (880)..(936)

<223> DAAO signature

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	ggg gtg atc ggg ctg acg acg gcc gtc gtc ctc gcc gag cgg ggc aga Gly Val Ile Gly Leu Thr Thr Ala Val Val Leu Ala Glu Arg Gly Arg 10 10 15 20	102
	cgg gtg cgg ctg tgg acc cgg gag ccc gcg gag cgg acc acc tcg gtg Arg Val Arg Leu Trp Thr Arg Glu Pro Ala Glu Arg Thr Thr Ser Val 25 30 35 40	150
15	gta gcg ggc ggg ctg tgg ccg tac cgg atc gag cgg gtc gcg ctg Val Ala Gly Gly Leu Trp Trp Pro Tyr Arg Ile Glu Pro Val Ala Leu 45 50 55	198
	gcc cag gcc tgg gcg ctg cgt tcc ctg gac gtg tac gag gag ctg gcg Ala Gln Ala Trp Ala Leu Arg Ser Leu Asp Val Tyr Glu Glu Leu Ala 60 65 70	246
20	gca cgg ccc ggg cag acc ggc gta cgc atg ctc gaa ggg gtg ctc ggc Ala Arg Pro Gly Gln Thr Gly Val Arg Met Leu Glu Gly Val Leu Gly 75 80 85	294
	gag acc ggc ctg gac gag gtg gac ggg tgg gcc gcg gcc cgg ctg ccc Glu Thr Gly Leu Asp Glu Val Asp Gly Trp Ala Ala Arg Leu Pro 90 95 100	342
25	ggg ctg cgc gcg agc gcc gag tac gac ggg acg ggg ctg tgg Gly Leu Arg Ala Ala Ser Ala Ala Glu Tyr Ala Gly Thr Gly Leu Trp 105 110 115 120	390
	gcg cgg ctg ccg ctc atc gac atg tcg acc cat ctg ccg tgg ctg cgg 30 Ala Arg Leu Pro Leu Ile Asp Met Ser Thr His Leu Pro Trp Leu Arg 125 130 135	438
	gag cgg ctg gcc gcg ggc acg gtg gag gac cgc gcg gtg acc Glu Arg Leu Leu Ala Ala Gly Gly Thr Val Glu Asp Arg Ala Val Thr 140 145 150	486
35	gat ctg gcc gag gcg gac gcg ccg gtg gtg gtc aac tgc acc ggc ctg Asp Leu Ala Glu Ala Asp Ala Pro Val Val Asn Cys Thr Gly Leu 155 160 165	534
	ggc gcc cgg gag ctg gtg ccg gac ccg gcg gta cgg ccg gtg cgc gga Gly Ala Arg Glu Leu Val Pro Asp Pro Ala Val Arg Pro Val Arg Gly 170 175 180	582
40	cag ctg gtc gtg gag aac ccc ggc atc cac aac tgg ctg gtc gcg Gln Leu Val Val Glu Asn Pro Gly Ile His Asn Trp Leu Val Ala 185 190 195 200	630
	gcc gac gcg gac tcc ggg gag acg acg tac ttc ctt ccg cag ccg gga 45 Ala Asp Ala Asp Ser Gly Glu Thr Thr Tyr Phe Leu Pro Gln Pro Gly 205 210 215	678
	cgg ctc ctg ctg ggc ggc acg gct gag gag gac gcc tgg tcg acc gag	726

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Arg Leu Leu Leu Gly Gly Thr Ala Glu Glu Asp Ala Trp Ser Thr Glu			
220	225	230	
ccg gac ccg gag gtc gcg gca atc gtg cga cgg tgc gcg gcc ctg			774
Pro Asp Pro Glu Val Ala Ala Ile Val Arg Arg Cys Ala Ala Leu			
5 235	240	245	
cgt ccc gag atc gcc gga gcg cgg gtg ctc gcg cac ctg gtg ggg ctg			822
Arg Pro Glu Ile Ala Gly Ala Arg Val Leu Ala His Leu Val Gly Leu			
250	255	260	
cgg ccg gcc cgg gac gcg gtc cgg ctg gag cgc ggg acg ctg ccg gac			870
10 Arg Pro Ala Arg Asp Ala Val Arg Leu Glu Arg Gly Thr Leu Pro Asp			
265	270	275	280
ggg cgc cgg ctg gtg cac aac tac ggt cac ggc ggc gcg ggc gtc acc			918
Gly Arg Arg Leu Val His Asn Tyr Gly His Gly Ala Gly Val Thr			
285	290	295	
15 gtg gcc tgg ggc tgc gct cag gag gcg gcc cgg ctc gcc tcctga			963
Val Ala Trp Gly Cys Ala Gln Glu Ala Ala Arg Leu Ala			
300	305		
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 35 Val Val Leu Ala Glu Arg Gly Arg Arg Val Arg Leu Trp Thr Arg Glu			
20 25 30			
Pro Ala Glu Arg Thr Thr Ser Val Val Ala Gly Gly Leu Trp Trp Pro			
35 40 45			
 40 Tyr Arg Ile Glu Pro Val Ala Leu Ala Gln Ala Trp Ala Leu Arg Ser			
50 55 60			
 45 Leu Asp Val Tyr Glu Glu Leu Ala Ala Arg Pro Gly Gln Thr Gly Val			
65 70 75 80			
Arg Met Leu Glu Gly Val Leu Gly Glu Thr Gly Leu Asp Glu Val Asp			
85 90 95			

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Gly Trp Ala Ala Ala Arg Leu Pro Gly Leu Arg Ala Ala Ser Ala Ala
100 105 110

5 Glu Tyr Ala Gly Thr Gly Leu Trp Ala Arg Leu Pro Leu Ile Asp Met
115 120 125

Ser Thr His Leu Pro Trp Leu Arg Glu Arg Leu Leu Ala Ala Gly Gly
130 135 140

10 Thr Val Glu Asp Arg Ala Val Thr Asp Leu Ala Glu Ala Asp Ala Pro
145 150 155 160

Val Val Val Asn Cys Thr Gly Leu Gly Ala Arg Glu Leu Val Pro Asp
165 170 175

15 Pro Ala Val Arg Pro Val Arg Gly Gln Leu Val Val Val Glu Asn Pro
180 185 190

Gly Ile His Asn Trp Leu Val Ala Ala Asp Ala Asp Ser Gly Glu Thr
20 195 200 205

Thr Tyr Phe Leu Pro Gln Pro Gly Arg Leu Leu Leu Gly Gly Thr Ala
210 215 220

25 Glu Glu Asp Ala Trp Ser Thr Glu Pro Asp Pro Glu Val Ala Ala Ala
225 230 235 240

Ile Val Arg Arg Cys Ala Ala Leu Arg Pro Glu Ile Ala Gly Ala Arg
245 250 255

30 Val Leu Ala His Leu Val Gly Leu Arg Pro Ala Arg Asp Ala Val Arg
260 265 270

Leu Glu Arg Gly Thr Leu Pro Asp Gly Arg Arg Leu Val His Asn Tyr
35 275 280 285

Gly His Gly Gly Ala Gly Val Thr Val Ala Trp Gly Cys Ala Gln Glu
290 295 300

40 Ala Ala Arg Leu Ala
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45 <212> DNA
<213> Candida boidinii

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1 5 10 15

10 act aca tac tgt tta atc tat gag gct gga tgt gct cca gct aaa att 96
Thr Thr Tyr Cys Leu Ile Tyr Glu Ala Gly Cys Ala Pro Ala Lys Ile
20 25 30

act att gtt gct gaa ttt tta cca ggt gat caa tct aca tta tat aca 144
Thr Ile Val Ala Glu Phe Leu Pro Gly Asp Gln Ser Thr Leu Tyr Thr
15 35 40 45

tct cca tgg gca ggt ggt aat ttt tct tgt att tca cca gct gat gat 192
Ser Pro Trp Ala Gly Gly Asn Phe Ser Cys Ile Ser Pro Ala Asp Asp
50 55 60

aca aca ttg gct tat gat aaa ttc aca tat ctt aat tta ttc aag att 240
20 Thr Thr Leu Ala Tyr Asp Lys Phe Thr Tyr Leu Asn Leu Phe Lys Ile
65 70 75 80

cac aaa aaa tta ggt gga cca gaa tgt gga tta gat aat aag cca agt 288
His Lys Lys Leu Gly Gly Pro Glu Cys Gly Leu Asp Asn Lys Pro Ser
85 90 95

25 act gaa tat tgg gat ttt tat cct ggt gat gaa aaa gtc aat tct tta 336
Thr Glu Tyr Trp Asp Phe Tyr Pro Gly Asp Glu Lys Val Asn Ser Leu
100 105 110

aaa caa tat ctt aaa gat ttt aaa gtt att cca aaa tca gaa tta cca 384
Lys Gln Tyr Leu Lys Asp Phe Lys Val Ile Pro Lys Ser Glu Leu Pro
30 115 120 125

gaa ggt gtt gaa tat ggt att agt tat act aca tgg aat ttc aac tgt 432
Glu Gly Val Glu Tyr Gly Ile Ser Tyr Thr Thr Trp Asn Phe Asn Cys
130 135 140

cct gtt ttc tta caa aat atg gct aat ttt tta aat aaa aga aat gtt 480
35 Pro Val Phe Leu Gln Asn Met Ala Asn Phe Leu Asn Lys Arg Asn Val
145 150 155 160

acc att att aga aaa cat tta aca cat att tct caa gct tat tta aca 528
Thr Ile Ile Arg Lys His Leu Thr His Ile Ser Gln Ala Tyr Leu Thr
165 170 175

40 gtt aat aca aaa gtt gtt ttc aac tgt aca ggt att ggt gct gct gat 576
Val Asn Thr Lys Val Val Phe Asn Cys Thr Gly Ile Gly Ala Ala Asp
180 185 190

tta ggt ggt gtt aaa gat gaa aaa gtt tat cca act aga gga caa gtt 624
Leu Gly Gly Val Lys Asp Glu Lys Val Tyr Pro Thr Arg Gly Gln Val
45 195 200 205

gtt gtt gtt aga gct cca cat att caa gaa aat aaa atg aga tgg ggt 672
Val Val Val Arg Ala Pro His Ile Gln Glu Asn Lys Met Arg Trp Gly

	210	215	220	
	aaa gac tat gct act tat att att cca aga cca tat tct aat ggt gaa			720
	Lys Asp Tyr Ala Thr Tyr Ile Ile Pro Arg Pro Tyr Ser Asn Gly Glu			
	225	230	235	240
5	tta gtc tta ggt ggt ttc tta caa aag gat aat tgg aca ggt aat act			768
	Leu Val Leu Gly Gly Phe Leu Gln Lys Asp Asn Trp Thr Gly Asn Thr			
	245	250	255	
	ttt ggt ttt gaa act gat gat att gtt agt aga act aca tct tta tta			816
	Phe Gly Phe Glu Thr Asp Asp Ile Val Ser Arg Thr Thr Ser Leu Leu			
10	260	265	270	
	cca aag att tta gat gaa cca ctt cat att att aga gtt gca gct ggt			864
	Pro Lys Ile Leu Asp Glu Pro Leu His Ile Ile Arg Val Ala Ala Gly			
	275	280	285	
	tta aga cca agt aga cat ggt ggt cca aga att gaa gct gaa gtt tgt			912
15	Leu Arg Pro Ser Arg His Gly Gly Pro Arg Ile Glu Ala Glu Val Cys			
	290	295	300	
	gaa gaa ggt aaa tta act att cat aat tat ggt gct tct gga tat ggt			960
	Glu Glu Gly Lys Leu Thr Ile His Asn Tyr Gly Ala Ser Gly Tyr Gly			
	305	310	315	320
20	tat caa gct ggt tat ggt atg tct tat gaa gct gtc aaa ctt tta gtt			1008
	Tyr Gln Ala Gly Tyr Gly Met Ser Tyr Glu Ala Val Lys Leu Leu Val			
	325	330	335	
	gat aac caa aaa gtt aaa gct aaa ctt tag			1038
	Asp Asn Gln Lys Val Lys Ala Lys Leu			
25	340	345		
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	20	25	30	
	Thr Ile Val Ala Glu Phe Leu Pro Gly Asp Gln Ser Thr Leu Tyr Thr			
40	35	40	45	
	Ser Pro Trp Ala Gly Gly Asn Phe Ser Cys Ile Ser Pro Ala Asp Asp			
	50	55	60	
45	Thr Thr Leu Ala Tyr Asp Lys Phe Thr Tyr Leu Asn Leu Phe Lys Ile			
	65	70	75	80

His Lys Lys Leu Gly Gly Pro Glu Cys Gly Leu Asp Asn Lys Pro Ser
85 90 95

5 Thr Glu Tyr Trp Asp Phe Tyr Pro Gly Asp Glu Lys Val Asn Ser Leu
100 105 110

Lys Gln Tyr Leu Lys Asp Phe Lys Val Ile Pro Lys Ser Glu Leu Pro
115 120 125

10 Glu Gly Val Glu Tyr Gly Ile Ser Tyr Thr Thr Trp Asn Phe Asn Cys
130 135 140

Pro Val Phe Leu Gln Asn Met Ala Asn Phe Leu Asn Lys Arg Asn Val
145 150 155 160

15 Thr Ile Ile Arg Lys His Leu Thr His Ile Ser Gln Ala Tyr Leu Thr
165 170 175

Val Asn Thr Lys Val Val Phe Asn Cys Thr Gly Ile Gly Ala Ala Asp
20 180 185 190

Leu Gly Gly Val Lys Asp Glu Lys Val Tyr Pro Thr Arg Gly Gln Val
195 200 205

25 Val Val Val Arg Ala Pro His Ile Gln Glu Asn Lys Met Arg Trp Gly
210 215 220

Lys Asp Tyr Ala Thr Tyr Ile Ile Pro Arg Pro Tyr Ser Asn Gly Glu
225 230 235 240

30 Leu Val Leu Gly Gly Phe Leu Gln Lys Asp Asn Trp Thr Gly Asn Thr
245 250 255

Phe Gly Phe Glu Thr Asp Asp Ile Val Ser Arg Thr Thr Ser Leu Leu
35 260 265 270

Pro Lys Ile Leu Asp Glu Pro Leu His Ile Ile Arg Val Ala Ala Gly
275 280 285

40 Leu Arg Pro Ser Arg His Gly Gly Pro Arg Ile Glu Ala Glu Val Cys
290 295 300

Glu Glu Gly Lys Leu Thr Ile His Asn Tyr Gly Ala Ser Gly Tyr Gly
305 310 315 320

45 Tyr Gln Ala Gly Tyr Gly Met Ser Tyr Glu Ala Val Lys Leu Leu Val
325 330 335

Asp Asn Gln Lys Val Lys Ala Lys Leu
340 345

- 5 <210> 15
<211> 12334
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- 10 <220>
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<223> Agrobacterium Right Border
- 15 <220>
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<222> (384) .. (639)
<223> complementary: NOS terminator
- 20 <220>
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<222> (716) .. (1822)
<223> complementary: coding for Rhodotorula gracilis DAAO
- 25 <220>
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<222> (1866) .. (3677)
<223> complementary: A.thaliana nitrilase I promoter
- 30 <220>
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